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SEQUENCE LISTING

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<120> METHODS AND COMPOSITIONS COMPRISING PROTEIN L IMMUNOGLOBULIN
BINDING DOMAINS FOR CELL-SPECIFIC TARGETING

<130> 9237.21WO

<160> 27

<170> PatentIn version 3.2

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Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp	
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Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr	
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Pro Gly Asn Glu Glu Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu	
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 35 40 45
 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
 50 55 60
 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
 65 70 75 80
 Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
 85 90 95
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Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr
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Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly Asn Glu Gln Lys Pro Gly
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Asn Glu Gln Lys Pro Asp Gln Pro Ser Lys Pro Glu Lys Glu Glu Asn
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gaa ttc aaa gga aca ttt gaa aaa gca aca tca gaa gct tat gcg tat 144
 Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala Tyr
 35 40 45

gca gat act ttg aag aaa gac aat gga gaa tat act gta gat gtt gca 192
 Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala
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 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 20 25 30
 aca ttt gaa gaa gca aca gca gaa gca tac aga tat gca gat gca tta 144
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 35 40 45
 aag aag gac aat gga gaa tat aca gta gac gtt gca gat aaa ggt tat 192
 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
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 act tta aat att aaa ttt gct gga 216
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 20 25 30

aca ttt gaa gaa gca aca gca gaa gca tac aga tat gct gac tta tta 144
 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45

gca aaa gaa aat ggt aaa tat aca gta gac gtt gca gat aaa ggt tat 192
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 20 25 30
 aca ttt gca gaa gca aca gca gaa gca tac aga tac gct gac tta tta 144
 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 35 40 45
 gca aaa gaa aat ggt aaa tat aca gca gac tta gaa gat ggt gga tac 192
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 1 5 10 15

 gaa aat ata tat ttt gaa gat gga aca gta caa act gca aca ttt aaa 96
 Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln Thr Ala Thr Phe Lys
 20 25 30

 gga aca ttt gca gaa gcg aca gca gaa gca tac aga tat gca gat ttg 144
 Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu
 35 40 45

 tta tca aaa gaa cat ggt aaa tac aca gca gac ttg gaa gat ggt gga 192
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 50 55 60

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 65 70

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 20 25 30

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 50 55 60

 Tyr Thr Ile Asn Ile Arg Phe Ala Gly
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 Ser Tyr Cys His His Thr Glu Pro Cys Phe Ser Pro Val Lys Ile Glu
 20 25 30
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 Gln Val Trp Asp Glu Ala Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser
 35 40 45
 gcc cag ttt gga tac gac caa agc gga gca gca agc gca aac aag tac 192
 Ala Gln Phe Gly Tyr Asp Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr
 50 55 60

cgc tac atg tcg ctt gag cag gat cac acc gtt aaa gaa ggc acc atg Arg Tyr Met Ser Leu Glu Gln Asp His Thr Val Lys Glu Gly Thr Met 65 70 75 80	240
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Ser Gly Lys Asn Ile Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Lys Thr
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Thr Asp His Leu Thr Leu Leu Thr Thr Arg Arg Leu Gly Ala Asn Pro
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Val Asp Arg Asp Gly Leu Glu Tyr Ile Trp Gly Asn His Glu Pro Val
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Arg Val Tyr Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro
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His Glu Ile Val Gln His Tyr Tyr His Arg His Pro Val Tyr Thr Ile
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Arg Cys Gly Ser Ser Gly Arg Ser Lys Arg Ser Val Ile Asp Asp Phe	
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acc ctg acc agc ccc tac ttg ggc aca tgc tcg tac tgc cac cat act	8696
Thr Leu Thr Ser Pro Tyr Leu Gly Thr Cys Ser Tyr Cys His His Thr	
75 80 85	
gta ccg tgc ttc agc cct gtt aag atc gag cag gtc tgg gac gaa gcg	8744
Val Pro Cys Phe Ser Pro Val Lys Ile Glu Gln Val Trp Asp Glu Ala	
90 95 100	
gac gat aac acc ata cgc ata cag act tcc gcc cag ttt gga tac gac	8792
Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser Ala Gln Phe Gly Tyr Asp	
105 110 115	
caa agc gga gca gca agc gca aac aag tac cgc tac atg tcg ctt aag	8840
Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr Arg Tyr Met Ser Leu Lys	
120 125 130	
cag gat cac acc gtt aaa gaa ggc acc atg gat gac atc aag att agc	8888
Gln Asp His Thr Val Lys Glu Gly Thr Met Asp Asp Ile Lys Ile Ser	
135 140 145 150	
acc tca gga ccg tgt aga agg ctt agc tac aaa gga tac ttt ctc ctc	8936
Thr Ser Gly Pro Cys Arg Arg Leu Ser Tyr Lys Gly Tyr Phe Leu Leu	
155 160 165	
gca aaa tgc cct cca ggg gac agc gta acg gtt agc ata gtg agt agc	8984
Ala Lys Cys Pro Pro Gly Asp Ser Val Thr Val Ser Ile Val Ser Ser	
170 175 180	
aac tca gca acg tca tgt aca ctg gcc cgc aag ata aaa cca aaa ttc	9032
Asn Ser Ala Thr Ser Cys Thr Leu Ala Arg Lys Ile Lys Pro Lys Phe	
185 190 195	
gtg gga cgg gaa aaa tat gat cta cct ccc gtt cac ggt aaa aaa att	9080
Val Gly Arg Glu Lys Tyr Asp Leu Pro Pro Val His Gly Lys Lys Ile	
200 205 210	
cct tgc aca gtg tac gac cgt ctg aaa gaa aca act gca ggc tac atc	9128
Pro Cys Thr Val Tyr Asp Arg Leu Lys Glu Thr Thr Ala Gly Tyr Ile	
215 220 225 230	

act atg cac agg ccg aga ccg cac gct tat aca tcc tac ctg gaa gaa	9176
Thr Met His Arg Pro Arg Pro His Ala Tyr Thr Ser Tyr Leu Glu Glu	
235 240 245	
tca tca ggg aaa gtt tac gca aag ccg cca tct ggg aag aac att acg	9224
Ser Ser Gly Lys Val Tyr Ala Lys Pro Pro Ser Gly Lys Asn Ile Thr	
250 255 260	
tat gag tgc aag tgc ggc gac tac aag acc gga acc gtt tcg acc cgc	9272
Tyr Glu Cys Lys Cys Gly Asp Tyr Lys Thr Gly Thr Val Ser Thr Arg	
265 270 275	
acc gaa atc act ggt tgc acc gcc atc aag cag tgc gtc gcc tat aag	9320
Thr Glu Ile Thr Gly Cys Thr Ala Ile Lys Gln Cys Val Ala Tyr Lys	
280 285 290	
agc gac caa acg aag tgg gtc ttc aac tca ccg gac ttg atc aga cat	9368
Ser Asp Gln Thr Lys Trp Val Phe Asn Ser Pro Asp Leu Ile Arg His	
295 300 305 310	
gac gac cac acg gcc caa ggg aaa ttg cat ttg cct ttc aag ttg atc	9416
Asp Asp His Thr Ala Gln Gly Lys Leu His Leu Pro Phe Lys Leu Ile	
315 320 325	
ccg agt acc tgc atg gtc cct gtt gcc cac gcg ccg aat gta ata cat	9464
Pro Ser Thr Cys Met Val Pro Val Ala His Ala Pro Asn Val Ile His	
330 335 340	
ggc ttt aaa cac atc agc ctc caa tta gat aca gac cac ttg aca ttg	9512
Gly Phe Lys His Ile Ser Leu Gln Leu Asp Thr Asp His Leu Thr Leu	
345 350 355	
ctc acc acc agg aga cta ggg gca aac ccg gaa cca acc act gaa tgg	9560
Leu Thr Thr Arg Arg Leu Gly Ala Asn Pro Glu Pro Thr Thr Glu Trp	
360 365 370	
atc gtc gga aag acg gtc aga aac ttc acc gtc gac cga gat ggc ctg	9608
Ile Val Gly Lys Thr Val Arg Asn Phe Thr Val Asp Arg Asp Gly Leu	
375 380 385 390	
gaa tac ata tgg gga aat cat gag cca gtg agg gtc tat gcc caa gag	9656
Glu Tyr Ile Trp Gly Asn His Glu Pro Val Arg Val Tyr Ala Gln Glu	
395 400 405	
tca gca cca gga gac cct cac gga tgg cca cac gaa ata gta cag cat	9704
Ser Ala Pro Gly Asp Pro His Gly Trp Pro His Glu Ile Val Gln His	
410 415 420	
tac tac cat cgc cat cct gtg tac acc atc tta gcc gtc gca tca gct	9752
Tyr Tyr His Arg His Pro Val Tyr Thr Ile Leu Ala Val Ala Ser Ala	
425 430 435	
acc gtg gcg atg atg att ggc gta act gtt gca gtg tta tgt gcc tgt	9800
Thr Val Ala Met Met Ile Gly Val Thr Val Ala Val Leu Cys Ala Cys	
440 445 450	
aaa gcg cgc cgt gag tgc ctg acg cca tac gcc ctg gcc cca aac gcc	9848

Lys	Ala	Arg	Arg	Glu	Cys	Leu	Thr	Pro	Tyr	Ala	Leu	Ala	Pro	Asn	Ala	
455					460					465					470	
gta atc cca act tcg ctg gca ctc ttg tgc tgc gtt agg tcg gcc aat 9896																
Val	Ile	Pro	Thr	Ser	Leu	Ala	Leu	Leu	Cys	Cys	Val	Arg	Ser	Ala	Asn	
				475					480					485		
gct gaaacgttca ccgagaccat gagttacttg tggtcgaaca gtcagccgtt 9949																
Ala																
cttctgggtc cagttgtgca tacctttggc cgctttcatc gttctaatagc gctgctgctc 10009																
ctgctgctg ccttttttag tggttgccgg cgcctacctg gcgaaggtag acgcctacga 10069																
acatgcgacc actgttccaa atgtgccaca gataccgtat aaggcacttg ttgaaagggc 10129																
agggatatgcc ccgctcaatt tggagatcac tgtcatgtcc tcggagggtt tgccttccac 10189																
caaccaagag tacattacct gcaaattcac cactgtgggc ccctcccaa aaatcaaagt 10249																
ctgcggctcc ttggaatgtc agccggccgc tcatgcagac tatacctgca aggtcttcgg 10309																
aggggtctac ccctttatgt ggggaggagc gcaatgtttt tgcgacagtg agaacagcca 10369																
gatgagtgag gcgtacgtcg aattgtcagc agattgcgcg tctgaccacg cgcaggcgat 10429																
taagggtgcac actgccgcga tgaaagtagg actgcgtatt gtgtacggga acactaccag 10489																
tttcttagat gtgtacgtga acggagtcac accaggaacg tctaaagact tgaaagtcac 10549																
agctggacca atttcagcat cgtttacgcc attcgatcat aaggtcgtta tccatcgcg 10609																
cctggtgtac aactatgact tcccgaata tggagcgatg aaaccaggag cgtttggaga 10669																
cattcaagct acctccttga ctagcaagga tctcatcgcc agcacagaca ttaggctact 10729																
caagccttcc gccagaacg tgcattgtccc gtacacgcag gcctcatcag gatttgagat 10789																
gtggaaaaac aactcaggcc gccactgca ggaaaccgca cctttcgggt gtaagattgc 10849																
agtaaateccg ctccgagcgg tggactgttc atacgggaac attcccattt ctattgacat 10909																
cccgaacgct gcctttatca ggacatcaga tgcaccactg gtctcaacag tcaaatgtga 10969																
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cgaccgcgaa ggtcaatgcc ccgtacattc gcattcgagc acagcaactc tccaagagtc 11089																
gacagtacat gtcttgagaa aaggagcggg gacagtacac tttagcaccg cgagtccaca 11149																
ggcgaacttt atcgatcgc tgtgtgggaa gaagacaaca tgcaatgcag aatgtaaacc 11209																
accagctgac catatcgtga gcaccccgca caaaaatgac caagaatttc aagccgccat 11269																
ctcaaaaaca tcatggagtt ggctgtttgc ccttttcggc ggcgcctcgt cgctattaat 11329																

tataggactt atgatttttg cttgcagcat gatgctgact agcacacgaa gatgaccgct 11389
 acgccccaat gatccgacca gcaaaactcg atgtacttcc gaggaactga tgtgcataat 11449
 gcatcaggct ggtacattag atccccgctt accgcgggca atatagcaac actaaaaact 11509
 cgatgtactt ccgaggaagc gcagtgcata atgctgcgca gtgttgccac ataaccacta 11569
 tattaaccat ttatctagcg gacgccaaaa actcaatgta tttctgagga agcgtggtgc 11629
 ataatgccac gcagcgtctg cataactttt attatttctt ttattaatca acaaaatttt 11689
 gtttttaaca tttc 11703

<210> 16
 <211> 64
 <212> PRT
 <213> Sindbis virus

<400> 16

Ser Ala Ala Pro Leu Val Thr Ala Met Cys Leu Leu Gly Asn Val Ser
 1 5 10 15

Phe Pro Cys Asp Arg Pro Pro Thr Cys Tyr Thr Arg Glu Pro Ser Arg
 20 25 30

Ala Leu Asp Ile Leu Glu Glu Asn Val Asn His Glu Ala Tyr Asp Thr
 35 40 45

Leu Leu Asn Ala Ile Leu Arg Cys Gly Ser Ser Gly Arg Ser Lys Arg
 50 55 60

<210> 17
 <211> 423
 <212> PRT
 <213> Sindbis virus

<400> 17

Ser Val Ile Asp Asp Phe Thr Leu Thr Ser Pro Tyr Leu Gly Thr Cys
 1 5 10 15

Ser Tyr Cys His His Thr Val Pro Cys Phe Ser Pro Val Lys Ile Glu
 20 25 30

Gln Val Trp Asp Glu Ala Asp Asp Asn Thr Ile Arg Ile Gln Thr Ser
 35 40 45

Ala Gln Phe Gly Tyr Asp Gln Ser Gly Ala Ala Ser Ala Asn Lys Tyr
50 55 60

Arg Tyr Met Ser Leu Lys Gln Asp His Thr Val Lys Glu Gly Thr Met
65 70 75 80

Asp Asp Ile Lys Ile Ser Thr Ser Gly Pro Cys Arg Arg Leu Ser Tyr
85 90 95

Lys Gly Tyr Phe Leu Leu Ala Lys Cys Pro Pro Gly Asp Ser Val Thr
100 105 110

Val Ser Ile Val Ser Ser Asn Ser Ala Thr Ser Cys Thr Leu Ala Arg
115 120 125

Lys Ile Lys Pro Lys Phe Val Gly Arg Glu Lys Tyr Asp Leu Pro Pro
130 135 140

Val His Gly Lys Lys Ile Pro Cys Thr Val Tyr Asp Arg Leu Lys Glu
145 150 155 160

Thr Thr Ala Gly Tyr Ile Thr Met His Arg Pro Arg Pro His Ala Tyr
165 170 175

Thr Ser Tyr Leu Glu Glu Ser Ser Gly Lys Val Tyr Ala Lys Pro Pro
180 185 190

Ser Gly Lys Asn Ile Thr Tyr Glu Cys Lys Cys Gly Asp Tyr Lys Thr
195 200 205

Gly Thr Val Ser Thr Arg Thr Glu Ile Thr Gly Cys Thr Ala Ile Lys
210 215 220

Gln Cys Val Ala Tyr Lys Ser Asp Gln Thr Lys Trp Val Phe Asn Ser
225 230 235 240

Pro Asp Leu Ile Arg His Asp Asp His Thr Ala Gln Gly Lys Leu His
245 250 255

Leu Pro Phe Lys Leu Ile Pro Ser Thr Cys Met Val Pro Val Ala His
260 265 270

Ala Pro Asn Val Ile His Gly Phe Lys His Ile Ser Leu Gln Leu Asp

275	280	285
Thr Asp His Leu Thr Leu Leu Thr Thr Arg Arg Leu Gly Ala Asn Pro		
290	295	300
Glu Pro Thr Thr Glu Trp Ile Val Gly Lys Thr Val Arg Asn Phe Thr		
305	310	315 320
Val Asp Arg Asp Gly Leu Glu Tyr Ile Trp Gly Asn His Glu Pro Val		
325	330	335
Arg Val Tyr Ala Gln Glu Ser Ala Pro Gly Asp Pro His Gly Trp Pro		
340	345	350
His Glu Ile Val Gln His Tyr Tyr His Arg His Pro Val Tyr Thr Ile		
355	360	365
Leu Ala Val Ala Ser Ala Thr Val Ala Met Met Ile Gly Val Thr Val		
370	375	380
Ala Val Leu Cys Ala Cys Lys Ala Arg Arg Glu Cys Leu Thr Pro Tyr		
385	390	395 400
Ala Leu Ala Pro Asn Ala Val Ile Pro Thr Ser Leu Ala Leu Leu Cys		
405	410	415
Cys Val Arg Ser Ala Asn Ala		
420		

<210> 18
 <211> 51
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Linker

<220>
 <221> CDS
 <222> (1)..(51)

<400> 18		
aga tct ggt ggc ggt ggc tcg ggc ggt ggt ggg tcg ggt ggc ggc gga		48
Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly		
1 5 10 15		

tct
Ser

51

<210> 19
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 19

Arg Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser

<210> 20
<211> 45
<212> DNA
<213> Artificial sequence

<220>
<223> Linker

<220>
<221> CDS
<222> (1) .. (45)

<400> 20
ggt ggc ggt ggc tcg ggc ggt ggt ggg tcg ggt ggc ggc gga tct 45
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 21
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 21

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 22

<211> 1050
 <212> DNA
 <213> Bluetongue virus 10

<220>
 <221> CDS
 <222> (1)..(1050)
 <223> VP7 gene

<400> 22

atg gac act atc gcc gca aga gca ctc act gtg atg cga gca tgt gct	48
Met Asp Thr Ile Ala Ala Arg Ala Leu Thr Val Met Arg Ala Cys Ala	
1 5 10 15	
acg ctt caa gag gca aga att gtg ttg gaa gcc aat gtg atg gaa att	96
Thr Leu Gln Glu Ala Arg Ile Val Leu Glu Ala Asn Val Met Glu Ile	
20 25 30	
ttg ggg ata gct atc aat agg tac aat gga ctc act tta cga gga gtg	144
Leu Gly Ile Ala Ile Asn Arg Tyr Asn Gly Leu Thr Leu Arg Gly Val	
35 40 45	
acg atg cgc ccg acc tcg tta gca caa aga aat gag atg ttt ttt atg	192
Thr Met Arg Pro Thr Ser Leu Ala Gln Arg Asn Glu Met Phe Phe Met	
50 55 60	
tgt ttg gat atg atg ctg tct gct gct ggg ata aat gtt gga ccg ata	240
Cys Leu Asp Met Met Leu Ser Ala Ala Gly Ile Asn Val Gly Pro Ile	
65 70 75 80	
tcg cca gac tat act caa cat atg gct acg att ggt gta cta gca aca	288
Ser Pro Asp Tyr Thr Gln His Met Ala Thr Ile Gly Val Leu Ala Thr	
85 90 95	
ccg gaa ata cct ttt aca acg gaa gcg gcg aat gaa ata gca cga gtg	336
Pro Glu Ile Pro Phe Thr Thr Glu Ala Ala Asn Glu Ile Ala Arg Val	
100 105 110	
act ggg gag act tcg aca tgg ggg cca gcg cgt cag cct tat ggt ttc	384
Thr Gly Glu Thr Ser Thr Trp Gly Pro Ala Arg Gln Pro Tyr Gly Phe	
115 120 125	
ttc ctt gaa act gag gaa acc ttc caa cca ggg agg tgg ttc atg cgc	432
Phe Leu Glu Thr Glu Glu Thr Phe Gln Pro Gly Arg Trp Phe Met Arg	
130 135 140	
gcc gct caa gca gta act gca gta gtg tgc ggt ccg gat atg att caa	480
Ala Ala Gln Ala Val Thr Ala Val Val Cys Gly Pro Asp Met Ile Gln	
145 150 155 160	
gtg tca ctt aat gct gga gcg aga gga gat gta caa cag ata ttt cag	528
Val Ser Leu Asn Ala Gly Ala Arg Gly Asp Val Gln Gln Ile Phe Gln	
165 170 175	
ggg cgt aat gat ccc atg atg ata tat tta gtg tgg agg aga atc gaa	576
Gly Arg Asn Asp Pro Met Met Ile Tyr Leu Val Trp Arg Arg Ile Glu	

180	185	190	
aac ttt gcg atg gcg caa ggt aat tca cag caa act caa gcg ggt gtg Asn Phe Ala Met Ala Gln Gly Asn Ser Gln Gln Thr Gln Ala Gly Val 195 200 205			624
act gtc agt gtt ggt gga gtt gac atg agg gcg gga cgc att ata gcg Thr Val Ser Val Gly Gly Val Asp Met Arg Ala Gly Arg Ile Ile Ala 210 215 220			672
tgg gat gga cag gcc gcg ctg cat gtg cat aat ccg aca caa cag aat Trp Asp Gly Gln Ala Ala Leu His Val His Asn Pro Thr Gln Gln Asn 225 230 235 240			720
gcg atg gtg caa ata cag gtt gtg ttc tat ata tct atg gat aaa act Ala Met Val Gln Ile Gln Val Val Phe Tyr Ile Ser Met Asp Lys Thr 245 250 255			768
tta aac cag tac ccc gct ttg act gct gag att ttc aat gtt tac agc Leu Asn Gln Tyr Pro Ala Leu Thr Ala Glu Ile Phe Asn Val Tyr Ser 260 265 270			816
ttc agg gac cac aca tgg cat ggg cta aga acg gcg ata tta aac aga Phe Arg Asp His Thr Trp His Gly Leu Arg Thr Ala Ile Leu Asn Arg 275 280 285			864
acc aca ctg cca aac atg ctg cca cca atc ttc cca cca aat gat cga Thr Thr Leu Pro Asn Met Leu Pro Pro Ile Phe Pro Pro Asn Asp Arg 290 295 300			912
gat agc atc tta act ctt cta ctt tta tct aca ctt gct gat gtt tac Asp Ser Ile Leu Thr Leu Leu Leu Leu Ser Thr Leu Ala Asp Val Tyr 305 310 315 320			960
act gtt tta agg cca gag ttt gcg att cac ggc gta aat ccg atg cca Thr Val Leu Arg Pro Glu Phe Ala Ile His Gly Val Asn Pro Met Pro 325 330 335			1008
ggg ccg ctc aca cgt gct att gcg cgc gcc gcc tat gtg tag Gly Pro Leu Thr Arg Ala Ile Ala Arg Ala Ala Tyr Val 340 345			1050

<210> 23
 <211> 349
 <212> PRT
 <213> Bluetongue virus 10

<400> 23

Met Asp Thr Ile Ala Ala Arg Ala Leu Thr Val Met Arg Ala Cys Ala
 1 5 10 15

Thr Leu Gln Glu Ala Arg Ile Val Leu Glu Ala Asn Val Met Glu Ile
 20 25 30

Leu Gly Ile Ala Ile Asn Arg Tyr Asn Gly Leu Thr Leu Arg Gly Val
 35 40 45

Thr Met Arg Pro Thr Ser Leu Ala Gln Arg Asn Glu Met Phe Phe Met
 50 55 60

Cys Leu Asp Met Met Leu Ser Ala Ala Gly Ile Asn Val Gly Pro Ile
 65 70 75 80

Ser Pro Asp Tyr Thr Gln His Met Ala Thr Ile Gly Val Leu Ala Thr
 85 90 95

Pro Glu Ile Pro Phe Thr Thr Glu Ala Ala Asn Glu Ile Ala Arg Val
 100 105 110

Thr Gly Glu Thr Ser Thr Trp Gly Pro Ala Arg Gln Pro Tyr Gly Phe
 115 120 125

Phe Leu Glu Thr Glu Glu Thr Phe Gln Pro Gly Arg Trp Phe Met Arg
 130 135 140

Ala Ala Gln Ala Val Thr Ala Val Val Cys Gly Pro Asp Met Ile Gln
 145 150 155 160

Val Ser Leu Asn Ala Gly Ala Arg Gly Asp Val Gln Gln Ile Phe Gln
 165 170 175

Gly Arg Asn Asp Pro Met Met Ile Tyr Leu Val Trp Arg Arg Ile Glu
 180 185 190

Asn Phe Ala Met Ala Gln Gly Asn Ser Gln Gln Thr Gln Ala Gly Val
 195 200 205

Thr Val Ser Val Gly Gly Val Asp Met Arg Ala Gly Arg Ile Ile Ala
 210 215 220

Trp Asp Gly Gln Ala Ala Leu His Val His Asn Pro Thr Gln Gln Asn
 225 230 235 240

Ala Met Val Gln Ile Gln Val Val Phe Tyr Ile Ser Met Asp Lys Thr
 245 250 255

Leu Asn Gln Tyr Pro Ala Leu Thr Ala Glu Ile Phe Asn Val Tyr Ser
 260 265 270

Phe Arg Asp His Thr Trp His Gly Leu Arg Thr Ala Ile Leu Asn Arg
 275 280 285

Thr Thr Leu Pro Asn Met Leu Pro Pro Ile Phe Pro Pro Asn Asp Arg
 290 295 300

Asp Ser Ile Leu Thr Leu Leu Leu Ser Thr Leu Ala Asp Val Tyr
 305 310 315 320

Thr Val Leu Arg Pro Glu Phe Ala Ile His Gly Val Asn Pro Met Pro
 325 330 335

Gly Pro Leu Thr Arg Ala Ile Ala Arg Ala Ala Tyr Val
 340 345

<210> 24
 <211> 585
 <212> DNA
 <213> *Coccidioides immitis*

<220>
 <221> CDS
 <222> (1) .. (585)
 <223> Ag2/PRA gene

<400> 24
 atg cag ttc tct cac gct ctc atc gct ctc gtc gct gcc ggc ctc gcc 48
 Met Gln Phe Ser His Ala Leu Ile Ala Leu Val Ala Ala Gly Leu Ala
 1 5 10 15
 agt gcc cag ctc cca gac atc cca cct tgc gct ctc aac tgc ttc gtt 96
 Ser Ala Gln Leu Pro Asp Ile Pro Pro Cys Ala Leu Asn Cys Phe Val
 20 25 30
 gag gct ctc ggc aac gat ggc tgc act cgc ttg acc gac ttc aag tgc 144
 Glu Ala Leu Gly Asn Asp Gly Cys Thr Arg Leu Thr Asp Phe Lys Cys
 35 40 45
 cac tgc tcc aag cct gag cta cca gga cag atc act cct tgc gtt gag 192
 His Cys Ser Lys Pro Glu Leu Pro Gly Gln Ile Thr Pro Cys Val Glu
 50 55 60
 gag gcc tgc cct ctc gac gcc cgt atc tcc gtc tcc aac atc gtc gtt 240
 Glu Ala Cys Pro Leu Asp Ala Arg Ile Ser Val Ser Asn Ile Val Val
 65 70 75 80
 gac cag tgc tcc aag gcc ggt gtc cca att gac atc cca cca gtt gac 288

Asp	Gln	Cys	Ser	Lys	Ala	Gly	Val	Pro	Ile	Asp	Ile	Pro	Pro	Val	Asp	
				85					90					95		
acc	acc	gcc	gct	ccc	gag	cca	tcc	gag	acc	gct	gag	ccc	acc	gct	gag	336
Thr	Thr	Ala	Ala	Pro	Glu	Pro	Ser	Glu	Thr	Ala	Glu	Pro	Thr	Ala	Glu	
				100				105					110			
cca	acc	gag	gag	ccc	act	gcc	gag	cct	acc	gct	gag	ccc	acc	gct	gag	384
Pro	Thr	Glu	Glu	Pro	Thr	Ala	Glu	Pro	Thr	Ala	Glu	Pro	Thr	Ala	Glu	
				115				120					125			
ccg	act	cat	gag	ccc	acc	gag	gag	ccc	act	gcc	gtc	cca	acc	ggc	act	432
Pro	Thr	His	Glu	Pro	Thr	Glu	Glu	Pro	Thr	Ala	Val	Pro	Thr	Gly	Thr	
				130				135				140				
ggc	ggt	ggt	gtc	ccc	act	ggc	acc	ggt	tcc	ttc	acc	gtc	act	ggc	aga	480
Gly	Gly	Gly	Val	Pro	Thr	Gly	Thr	Gly	Ser	Phe	Thr	Val	Thr	Gly	Arg	
				145				150				155			160	
cca	act	gcc	tcc	acc	cca	gct	gag	ttc	cca	ggt	gct	ggc	tcc	aac	gtc	528
Pro	Thr	Ala	Ser	Thr	Pro	Ala	Glu	Phe	Pro	Gly	Ala	Gly	Ser	Asn	Val	
				165				170						175		
cgt	gcc	agc	gtt	ggc	ggc	att	gct	gct	gct	ctc	ctc	ggt	ctc	gct	gcc	576
Arg	Ala	Ser	Val	Gly	Gly	Ile	Ala	Ala	Ala	Leu	Leu	Gly	Leu	Ala	Ala	
				180				185						190		
tac	ctg	taa														585
Tyr	Leu															

<210> 25
 <211> 194
 <212> PRT
 <213> Coccidioides immitis

<400> 25

Met	Gln	Phe	Ser	His	Ala	Leu	Ile	Ala	Leu	Val	Ala	Ala	Gly	Leu	Ala	
1				5					10					15		
Ser	Ala	Gln	Leu	Pro	Asp	Ile	Pro	Pro	Cys	Ala	Leu	Asn	Cys	Phe	Val	
			20					25					30			
Glu	Ala	Leu	Gly	Asn	Asp	Gly	Cys	Thr	Arg	Leu	Thr	Asp	Phe	Lys	Cys	
			35				40					45				
His	Cys	Ser	Lys	Pro	Glu	Leu	Pro	Gly	Gln	Ile	Thr	Pro	Cys	Val	Glu	
	50					55					60					
Glu	Ala	Cys	Pro	Leu	Asp	Ala	Arg	Ile	Ser	Val	Ser	Asn	Ile	Val	Val	
65					70				75					80		

Asp Gln Cys Ser Lys Ala Gly Val Pro Ile Asp Ile Pro Pro Val Asp
 85 90 95

Thr Thr Ala Ala Pro Glu Pro Ser Glu Thr Ala Glu Pro Thr Ala Glu
 100 105 110

Pro Thr Glu Glu Pro Thr Ala Glu Pro Thr Ala Glu Pro Thr Ala Glu
 115 120 125

Pro Thr His Glu Pro Thr Glu Glu Pro Thr Ala Val Pro Thr Gly Thr
 130 135 140

Gly Gly Gly Val Pro Thr Gly Thr Gly Ser Phe Thr Val Thr Gly Arg
 145 150 155 160

Pro Thr Ala Ser Thr Pro Ala Glu Phe Pro Gly Ala Gly Ser Asn Val
 165 170 175

Arg Ala Ser Val Gly Gly Ile Ala Ala Ala Leu Leu Gly Leu Ala Ala
 180 185 190

Tyr Leu

<210> 26
 <211> 906
 <212> DNA
 <213> Streptococcus pneumoniae

<220>
 <221> CDS
 <222> (1)..(906)
 <223> PspA gene

<400> 26
 gaa gaa tct ccc gta gcc agt cag tct aaa gct gag aaa gac tat gat 48
 Glu Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp
 1 5 10 15

gca gcg aag aaa gat gct aag aat gcg aaa aaa gca gta gaa gat gct 96
 Ala Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala
 20 25 30

caa aag gct tta gat gat gca aaa gct gct cag aaa aaa tat gac gag 144
 Gln Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu
 35 40 45

gat cag aag aaa act gag gag aaa gcc gcg cta gaa aaa gca gcg tct Asp Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser 50 55 60	192
gaa gag atg gat aag gca gtg gca gca gtt caa caa gcg tat cta gcc Glu Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala 65 70 75 80	240
tat caa caa gct aca gac aaa gcc gca aaa gac gca gca gat aag atg Tyr Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met 85 90 95	288
ata gat gaa gct aag aaa cgc gaa gaa gag gca aaa act aaa ttt aat Ile Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn 100 105 110	336
act gtt cga gca atg gta gtt cct gag cca gag cag ttg gct gag act Thr Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr 115 120 125	384
aag aaa aaa tca gaa gaa gct aaa caa aaa gca cca gaa ctt act aaa Lys Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys 130 135 140	432
aaa cta gaa gaa gct aaa gca aaa tta gaa gag gct gag aaa aaa gct Lys Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala 145 150 155 160	480
act gaa gcc aaa caa aaa gtg gat gct gaa gaa gtc gct cct caa gct Thr Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala 165 170 175	528
aaa atc gct gaa ttg gaa aat caa gtt cat aga cta gaa caa gag ctc Lys Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu 180 185 190	576
aaa gag att gat gag tct gaa tca gaa gat tat gct aaa gaa ggt ttc Lys Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe 195 200 205	624
cgt gct cct ctt caa tct aaa ttg gat gcc aaa aaa gct aaa cta tca Arg Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser 210 215 220	672
aaa ctt gaa gag tta agt gat aag att gat gag tta gac gct gaa att Lys Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile 225 230 235 240	720
gca aaa ctt gaa gat caa ctt aaa gct gct gaa gaa aac aat aat gta Ala Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Asn Val 245 250 255	768
gaa gac tac ttt aaa gaa ggt tta gag aaa act att gct gct aaa aaa Glu Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys 260 265 270	816

gct gaa tta gaa aaa act gaa gct gac ctt aag aaa gca gtt aat gag 864
 Ala Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu
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<210> 27

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<212> PRT

<213> Streptococcus pneumoniae

<400> 27

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Ala Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala
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Gln Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu
 35 40 45

Asp Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser
 50 55 60

Glu Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala
 65 70 75 80

Tyr Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met
 85 90 95

Ile Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn
 100 105 110

Thr Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr
 115 120 125

Lys Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys
 130 135 140

Lys Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala
 145 150 155 160

Thr Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala

	165		170		175										
Lys	Ile	Ala	Glu	Leu	Glu	Asn	Gln	Val	His	Arg	Leu	Glu	Gln	Glu	Leu
			180					185					190		
Lys	Glu	Ile	Asp	Glu	Ser	Glu	Ser	Glu	Asp	Tyr	Ala	Lys	Glu	Gly	Phe
			195					200					205		
Arg	Ala	Pro	Leu	Gln	Ser	Lys	Leu	Asp	Ala	Lys	Lys	Ala	Lys	Leu	Ser
			210					215					220		
Lys	Leu	Glu	Glu	Leu	Ser	Asp	Lys	Ile	Asp	Glu	Leu	Asp	Ala	Glu	Ile
			225					230				235			240
Ala	Lys	Leu	Glu	Asp	Gln	Leu	Lys	Ala	Ala	Glu	Glu	Asn	Asn	Asn	Val
				245						250				255	
Glu	Asp	Tyr	Phe	Lys	Glu	Gly	Leu	Glu	Lys	Thr	Ile	Ala	Ala	Lys	Lys
			260							265				270	
Ala	Glu	Leu	Glu	Lys	Thr	Glu	Ala	Asp	Leu	Lys	Lys	Ala	Val	Asn	Glu
			275					280					285		
Pro	Glu	Lys	Pro	Ala	Pro	Ala	Pro	Glu	Thr	Pro	Ala	Pro	Glu		
			290					295					300		